

J. Hunt

APPLICANT'S COPY

BIOTECHNOLOGY
SYSTEMS
BRANCH



**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/506,079C
Source: 1600
Date Processed by STIC: 8/14/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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SERIAL NUMBER: 09/506,079C

1. _____ Wrapped Nucleics: The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
 . _____ Wrapped Aminos:

3. _____ Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. -

5 _____ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

7 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

8 Skipped Sequences Sequence(s) missing. If intentional; please insert the following lines for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000

10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

12 _____ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/506,079C

DATE: 08/14/2001

TIME: 16:50:47

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\08142001\I506079C.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Clinton, Gail M.
 4 Evans, Adam
 5 Henner, William D.
 7 <120> TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
 9 <130> FILE REFERENCE: 49321-16
 11 <140> CURRENT APPLICATION NUMBER: US 09/506,079C
 OK 12 <141> CURRENT FILING DATE: 2000-02-16
 14 <150> PRIOR APPLICATION NUMBER: US 09/234,208
 15 <151> PRIOR FILING DATE: 1999-01-20
 17 <160> NUMBER OF SEQ ID NOS: 10

ERRORED SEQUENCES

249 <210> SEQ ID NO: 10
 250 <211> LENGTH: 240
 251 <212> TYPE: DNA
 252 <213> ORGANISM: Homo Sapiens
 254 <400> SEQUENCE: 10
 255 ggt wcc cac tca cyg cgc ccg agg cca gct gca gtt cct gtc cct 45
 OK 256 Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro
 257 5 10 15
 E--> 259 cwg cgc atr cag cct ggc cca gcc cac cct gtc cta tcc ttc ctc 90
 OK 260 Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu
 261 20 25 30
 263 aga ccc tct tgg gac mta gtc tct gcc ttc tac tct cta ccc ctg 135
 OK 264 Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu
 265 35 40 45
 267 gcc ccc ctc agc cct aca agt gtc cst ata tcc cct gtc agt gtg 180
 OK 268 Ala Pro Leu Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
 269 50 55 60
 271 ggg agg ggc cyg gac cct gat gct cat gtg gct gtt sac ctg tcc 225
 OK 272 Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser
 273 65 70 75
 275 cgg tat gaa ggc tga 240
 276 Arg Tyr Glu Gly
 W--> 286 ⑦ delete at end of file

see item 9
 in Encl
 Summary Sheet

PSL →

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

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VERIFICATION SUMMARY

DATE: 08/14/2001

PATENT APPLICATION: US/09/506,079C

TIME: 16:50:48

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\08142001\I506079C.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:27 M:283 W: Missing Blank Line separator, <220> field identifier
L:31 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:283 W: Missing Blank Line separator, <220> field identifier
L:39 M:283 W: Missing Blank Line separator, <220> field identifier
L:43 M:283 W: Missing Blank Line separator, <220> field identifier
L:48 M:283 W: Missing Blank Line separator, <220> field identifier
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:283 W: Missing Blank Line separator, <220> field identifier
L:60 M:283 W: Missing Blank Line separator, <220> field identifier
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:82 M:283 W: Missing Blank Line separator, <220> field identifier
L:86 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:283 W: Missing Blank Line separator, <220> field identifier
L:94 M:283 W: Missing Blank Line separator, <220> field identifier
L:98 M:283 W: Missing Blank Line separator, <220> field identifier
L:102 M:283 W: Missing Blank Line separator, <220> field identifier
L:107 M:283 W: Missing Blank Line separator, <220> field identifier
L:111 M:283 W: Missing Blank Line separator, <220> field identifier
L:115 M:283 W: Missing Blank Line separator, <220> field identifier
L:119 M:283 W: Missing Blank Line separator, <220> field identifier
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:183 M:283 W: Missing Blank Line separator, <220> field identifier
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:203 M:283 W: Missing Blank Line separator, <220> field identifier
L:213 M:283 W: Missing Blank Line separator, <220> field identifier
L:223 M:283 W: Missing Blank Line separator, <220> field identifier
L:233 M:283 W: Missing Blank Line separator, <220> field identifier
L:243 M:283 W: Missing Blank Line separator, <220> field identifier
L:256 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10

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